



Sequence Listing

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Baker, Kevin P.
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Gurney, Austin
Kim, Kyung Jin
Wood, William I.

<120> Apo-2DcR

<130> P1110P1

<140> US 09/096,500

<141> 1998-06-12

<150> US 60/049,911

<151> 1997-06-18

<160> 17

<210> 1

<211> 259

<212> PRT

<213> Homo sapiens

<400> 1

Met Ala Arg Ile Pro Lys Thr Leu Lys Phe Val Val Val Ile Val
1 5 10 15

Ala Val Leu Leu Pro Val Leu Ala Tyr Ser Ala Thr Thr Ala Arg
20 25 30

Gln Glu Glu Val Pro Gln Gln Thr Val Ala Pro Gln Gln Gln Arg
35 40 45

His Ser Phe Lys Gly Glu Glu Cys Pro Ala Gly Ser His Arg Ser
50 55 60

Glu His Thr Gly Ala Cys Asn Pro Cys Thr Glu Gly Val Asp Tyr
65 70 75

Thr Asn Ala Ser Asn Asn Glu Pro Ser Cys Phe Pro Cys Thr Val
80 85 90

Cys Lys Ser Asp Gln Lys His Lys Ser Ser Cys Thr Met Thr Arg
95 100 105

Asp Thr Val Cys Gln Cys Lys Glu Gly Thr Phe Arg Asn Glu Asn
110 115 120

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Ser Pro Glu Met Cys Arg Lys Cys Ser Arg Cys Pro Ser Gly Glu
125 130 135

Val Gln Val Ser Asn Cys Thr Ser Trp Asp Asp Ile Gln Cys Val
140 145 150

Glu Glu Phe Gly Ala Asn Ala Thr Val Glu Thr Pro Ala Ala Glu
155 160 165

Glu Thr Met Asn Thr Ser Pro Gly Thr Pro Ala Pro Ala Ala Glu
170 175 180

Glu Thr Met Asn Thr Ser Pro Gly Thr Pro Ala Pro Ala Ala Glu
185 190 195

Glu Thr Met Thr Thr Ser Pro Gly Thr Pro Ala Pro Ala Ala Glu
200 205 210

Glu Thr Met Thr Thr Ser Pro Gly Thr Pro Ala Pro Ala Ala Glu
215 220 225

Glu Thr Met Thr Thr Ser Pro Gly Thr Pro Ala Ser Ser His Tyr
230 235 240

Leu Ser Cys Thr Ile Val Gly Ile Ile Val Leu Ile Val Leu Leu
245 250 255

Ile Val Phe Val

<210> 2
<211> 1180
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (193) . . . (969)
<223>

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attttggaa gtttgaccag agatgcaagg ggtgaaggag cgtttcctac 100

cgtagggaa ctctggggac agagcgcccc ggccgcctga tggccgaggc 150

agggtgcac ccaggaccca ggacggcgac gggaaaccata cc atg 195
Met
1

gcc cg_g atc ccc aag acc cta aag ttc gtc gtc gtc atc 234
Ala Arg Ile Pro Lys Thr Leu Lys Phe Val Val Val Ile
5 10

gtc g_c gtc ctg ctg cca gtc cta gct tac tct gcc acc 273
Val Ala Val Leu Leu Pro Val Leu Ala Tyr Ser Ala Thr
15 20 25

act gcc cg_g cag gag gaa gtt ccc cag cag aca gtg gcc 312
Thr Ala Arg Gln Glu Glu Val Pro Gln Gln Thr Val Ala
30 35 40

cca cag caa cag agg cac agc ttc aag ggg gag gag tgt 351
Pro Gln Gln Arg His Ser Phe Lys Gly Glu Glu Cys
45 50

cca gca gga tct cat aga tca gaa cat act gga gcc tgt 390
Pro Ala Gly Ser His Arg Ser Glu His Thr Gly Ala Cys
55 60 65

aac ccg tgc aca gag ggt gtg gat tac acc aac gct tcc 429
Asn Pro Cys Thr Glu Gly Val Asp Tyr Thr Asn Ala Ser
70 75

aac aat gaa cct tct tgc ttc cca tgt aca gtt tgt aaa 468
Asn Asn Glu Pro Ser Cys Phe Pro Cys Thr Val Cys Lys
80 85 90

tca gat caa aaa cat aaa agt tcc tgc acc atg acc acc aga 507
Ser Asp Gln Lys His Lys Ser Ser Cys Thr Met Thr Arg
95 100 105

gac aca gtg tgt cag tgt aaa gaa ggc acc ttc cg_g aat 546
Asp Thr Val Cys Gln Cys Lys Glu Gly Thr Phe Arg Asn
110 115

gaa aac tcc cca gag atg tgc cg_g aag tgt agc agg tgc 585
Glu Asn Ser Pro Glu Met Cys Arg Lys Cys Ser Arg Cys
120 125 130

cct agt ggg gaa gtc caa gtc agt aat tgt acg tcc tgg 624
Pro Ser Gly Glu Val Gln Val Ser Asn Cys Thr Ser Trp
135 140

gat gat atc cag tgt gtt gaa gaa ttt ggt gcc aat gcc 663
Asp Asp Ile Gln Cys Val Glu Glu Phe Gly Ala Asn Ala
145 150 155

act gtg gaa acc cca gct gct gaa gag aca atg aac acc 702
Thr Val Glu Thr Pro Ala Ala Glu Glu Thr Met Asn Thr
160 165 170

agc ccg ggg act cct gcc cca gct gct gaa gag aca atg 741
Ser Pro Gly Thr Pro Ala Pro Ala Ala Glu Glu Thr Met
175 180

aac acc agc cca ggg act cct gcc cca gct gct gaa gag 780
Asn Thr Ser Pro Gly Thr Pro Ala Pro Ala Ala Glu Glu
185 190 195

aca atg acc acc agc ccg ggg act cct gcc cca gct gct 819
Thr Met Thr Ser Pro Gly Thr Pro Ala Pro Ala Ala
200 205

gaa gag aca atg acc acc agc ccg ggg act cct gcc cca 858
Glu Glu Thr Met Thr Ser Pro Gly Thr Pro Ala Pro
210 215 220

gct gct gaa gag aca atg acc acc agc ccg ggg act cct 897
Ala Ala Glu Glu Thr Met Thr Ser Pro Gly Thr Pro
225 230 235

gcc tct tct cat tac ctc tca tgc acc atc gta ggg atc 936
Ala Ser Ser His Tyr Leu Ser Cys Thr Ile Val Gly Ile
240 245

ata gtt cta att gtg ctt ctg att gtg ttt gtt t 970
Ile Val Leu Ile Val Leu Leu Ile Val Phe Val
250 255 259

gaaagacttc actgtggaag aaattccttc cttacctgaa aggttcaggt 1020

aggcgctggc tgagggcggg gggcgctgga cactctctgc cctgcctccc 1070

tctgctgtgt tcccacagac agaaacgcct gcccctgccc caaaaaaaaa 1120

aaaaaaaaaaa aaaaaaaaaaaa aaaaaaaaaaaa aaaaaaaaaaaa 1170

aaaaaaaaaaa 1180

<210> 3

<211> 299

<212> PRT

<213> Homo sapiens

<400> 3

Met Gln Gly Val Lys Glu Arg Phe Leu Pro Leu Gly Asn Ser Gly
1 5 10 15

Asp Arg Ala Pro Arg Pro Pro Asp Gly Arg Gly Arg Val Arg Pro
20 25 30

Arg Thr Gln Asp Gly Val Gly Asn His Thr Met Ala Arg Ile Pro
35 40 45
Lys Thr Leu Lys Phe Val Val Val Ile Val Ala Val Leu Leu Pro
50 55 60
Val Leu Ala Tyr Ser Ala Thr Thr Ala Arg Gln Glu Glu Val Pro
65 70 75
Gln Gln Thr Val Ala Pro Gln Gln Gln Arg His Ser Phe Lys Gly
80 85 90
Glu Glu Cys Pro Ala Gly Ser His Arg Ser Glu His Thr Gly Ala
95 100 105
Cys Asn Pro Cys Thr Glu Gly Val Asp Tyr Thr Asn Ala Ser Asn
110 115 120
Asn Glu Pro Ser Cys Phe Pro Cys Thr Val Cys Lys Ser Asp Gln
125 130 135
Lys His Lys Ser Ser Cys Thr Met Thr Arg Asp Thr Val Cys Gln
140 145 150
Cys Lys Glu Gly Thr Phe Arg Asn Glu Asn Ser Pro Glu Met Cys
155 160 165
Arg Lys Cys Ser Arg Cys Pro Ser Gly Glu Val Gln Val Ser Asn
170 175 180
Cys Thr Ser Trp Asp Asp Ile Gln Cys Val Glu Glu Phe Gly Ala
185 190 195
Asn Ala Thr Val Glu Thr Pro Ala Ala Glu Glu Thr Met Asn Thr
200 205 210
Ser Pro Gly Thr Pro Ala Pro Ala Ala Glu Glu Thr Met Asn Thr
215 220 225
Ser Pro Gly Thr Pro Ala Pro Ala Ala Glu Glu Thr Met Thr Thr
230 235 240
Ser Pro Gly Thr Pro Ala Pro Ala Ala Glu Glu Thr Met Thr Thr
245 250 255
Ser Pro Gly Thr Pro Ala Pro Ala Ala Glu Glu Thr Met Thr Thr
260 265 270
Ser Pro Gly Thr Pro Ala Ser Ser His Tyr Leu Ser Cys Thr Ile
275 280 285

Val Gly Ile Ile Val Leu Ile Val Leu Leu Ile Val Phe Val
290 295

<210> 4

<211> 1180

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (73) . . . (969)

<223>

<220>

<221> sig_peptide

<222> (73) . . . (194)

<223>

<400> 4

gctgtggaa cctctccacg cgcacgaact cagccaacga tttctgatag 50

atttttggga gtttgaccag ag atg caa ggg gtg aag gag 90
Met Gln Gly Val Lys Glu
-40 -35

cgc ttc cta ccg tta ggg aac tct ggg gac aga gcg ccc 129
Arg Phe Leu Pro Leu Gly Asn Ser Gly Asp Arg Ala Pro
-30 -25

cgg ccg cct gat ggc cga ggc agg gtg cga ccc agg acc 168
Arg Pro Pro Asp Gly Arg Gly Val Arg Pro Arg Thr
-20 -15 -10

cag gac ggc gtc ggg aac cat acc atg gcc cgg atc ccc 207
Gln Asp Gly Val Gly Asn His Thr Met Ala Arg Ile Pro
-5 1 5

aag acc cta aag ttc gtc gtc atc gtc gtc gtc ctg 246
Lys Thr Leu Lys Phe Val Val Val Ile Val Ala Val Leu
10 15

ctg cca gtc cta gct tac tct gcc acc act gcc cgg cag 285
Leu Pro Val Leu Ala Tyr Ser Ala Thr Thr Ala Arg Gln
20 25 30

gag gaa gtt ccc cag cag aca gtg gcc cca cag caa cag 324
Glu Glu Val Pro Gln Gln Thr Val Ala Pro Gln Gln Gln
35 40

agg cac agc ttc aag ggg gag gag tgt cca gca gga tct 363
Arg His Ser Phe Lys Gly Glu Glu Cys Pro Ala Gly Ser

45

50

55

cat aga tca gaa cat act gga gcc tgt aac ccg tgc aca 402
His Arg Ser Glu His Thr Gly Ala Cys Asn Pro Cys Thr
60 65 70

gag ggt gtg gat tac acc aac gct tcc aac aat gaa cct 441
Glu Gly Val Asp Tyr Thr Asn Ala Ser Asn Asn Glu Pro
75 80

tct tgc ttc cca tgt aca gtt tgt aaa tca gat caa aaa 480
Ser Cys Phe Pro Cys Thr Val Cys Lys Ser Asp Gln Lys
85 90 95

cat aaa agt tcc tgc acc atg acc aga gac aca gtg tgt 519
His Lys Ser Ser Cys Thr Met Thr Arg Asp Thr Val Cys
100 105

cag tgt aaa gaa ggc acc ttc cg^g aat gaa aac tcc cca 558
Gln Cys Lys Glu Gly Thr Phe Arg Asn Glu Asn Ser Pro
110 115 120

gag atg tgc cg^g aag tgt agc agg tgc cct agt ggg gaa 597
Glu Met Cys Arg Lys Cys Ser Arg Cys Pro Ser Gly Glu
125 130 135

gtc caa gtc agt aat tgt acg tcc tgg gat gat atc cag 636
Val Gln Val Ser Asn Cys Thr Ser Trp Asp Asp Ile Gln
140 145

tgt gtt gaa gaa ttt ggt gcc aat gcc act gtg gaa acc 675
Cys Val Glu Glu Phe Gly Ala Asn Ala Thr Val Glu Thr
150 155 160

cca gct gct gaa gag aca atg aac acc agc ccg ggg act 714
Pro Ala Ala Glu Glu Thr Met Asn Thr Ser Pro Gly Thr
165 170

cct gcc cca gct gct gaa gag aca atg aac acc agc cca 753
Pro Ala Pro Ala Glu Glu Thr Met Asn Thr Ser Pro
175 180 185

ggg act cct gcc cca gct gct gaa gag aca atg acc acc 792
Gly Thr Pro Ala Pro Ala Ala Glu Glu Thr Met Thr Thr
190 195 200

agc ccg ggg act cct gcc cca gct gct gaa gag aca atg 831
Ser Pro Gly Thr Pro Ala Pro Ala Ala Glu Glu Thr Met
205 210

acc acc agc ccg ggg act cct gcc cca gct gct gaa gag 870

Thr Thr Ser Pro Gly Thr Pro Ala Pro Ala Ala Glu Glu
215 220 225

aca atg acc acc agc ccg ggg act cct gcc tct tct cat 909
Thr Met Thr Thr Ser Pro Gly Thr Pro Ala Ser Ser His
230 235

tac ctc tca tgc acc atc gta ggg atc ata gtt cta att 948
Tyr Leu Ser Cys Thr Ile Val Gly Ile Ile Val Leu Ile
240 245 250

gtg ctt ctg att gtg ttt gtt t gaaagacttc actgtggaag 990
Val Leu Leu Ile Val Phe Val
255 259

aaattccttc cttacctgaa aggttcaggt aggcgctggc tgagggcggg 1040

ggcgctgga cactctctgc cctgcctccc tctgctgtgt tcccacagac 1090

agaaacgcct gcccctgccc caaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1140

aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1180

<210> 5

<211> 43

<212> DNA

<213> Yeast

<400> 5

tgtaaaacga cggccaggtt aatagacctg caattattaa tct 43

<210> 6

<211> 41

<212> DNA

<213> Yeast

<400> 6

caggaaacag ctatgaccac ctgcacacacct gcaaatccat t 41

<210> 7

<211> 49

<212> PRT

<213> Homo sapiens

<400> 7

Cys Arg Glu Cys Glu Ser Gly Ser Phe Thr Ala Ser Glu Asn His
1 5 10 15

Leu Arg His Cys Leu Ser Cys Ser Lys Cys Arg Lys Glu Met Gly
20 25 30

Gln Val Glu Ile Ser Ser Cys Thr Val Asp Arg Asp Thr Val Cys
35 40 45

Gly Cys Arg Lys

<210> 8

<211> 48

<212> PRT

<213> Homo sapiens

<400> 8

Cys Asn Pro Cys Thr Glu Gly Val Asp Tyr Thr Asn Ala Ser Asn
1 5 10 15

Asn Glu Pro Ser Cys Phe Pro Cys Thr Val Cys Lys Ser Asp Gln
20 25 30

Lys His Lys Ser Ser Cys Thr Met Thr Arg Asp Thr Val Cys Gln
35 40 45

Cys Lys Glu

<210> 9

<211> 70

<212> DNA

<213> Homo sapiens

<400> 9

gggagccgct catgaggaag ttgggcctca tggacaatga gataaaggtg 50

gctaaagctg aggcagcggg 70

<210> 10

<211> 1799

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (140) . . . (1372)

<223>

<220>

<221> Unsure

<222> 1367

<223> W may be adenine or thymine or uracil

<400> 10

cccacgcgtc cgcataaatac agcacgcggc cggagaaccc cgcaatctct 50

gcgcccacaa aatacaccga cgatgcccga tctactttaa gggctgaaac 100
ccacgggcct gagagactat aagagcggttc cctaccgcca tggaaacaacg 150
gggacagaac gcicccggccg cttcgggggc ccggaaaagg cacggcccag 200
gaccaggga ggcgcgggga gccaggcctg ggctccgggt ccccaagacc 250
cttgtgctcg ttgtcgccgc ggtcctgctg ttggtctcag ctgagttctgc 300
tctgatcacc caacaagacc tagctccccca gcagagagcg gccccacaac 350
aaaagaggtc cagcccctca gagggattgt gtccacactgg acaccatatc 400
tcagaagacg gtagagattg catctcctgc aaatatggac aggactatag 450
cactcactgg aatgacactcc ttttctgctt gcgctgcacc aggttgatt 500
caggtgaagt ggagctaagt ccctgcacca cgaccagaaa cacagtgtgt 550
cagtgcgaag aaggcacctt ccgggaagaa gattctcctg agatgtgccc 600
gaagtgccgc acagggtgtc ccagagggat ggtcaagggtc ggtgattgt 650
caccctggag tgacatcgaa tgtgtccaca aagaatcagg catcatcata 700
ggagtcacag ttgcagccgt agtcttgatt gtggctgtgt ttgtttgcaa 750
gtctttactg tggaaagaaag tccttcctta cctgaaaggc atctgctcag 800
gtggtggtgg ggaccctgag cgtgtggaca gaagctcaca acgacactggg 850
gctgaggaca atgtcctcaa tgagatcgtg agtatcttgc agcccaccca 900
ggtccctgag cagaaatgg aagtccagga gccagcagag ccaacaggtg 950
tcaacatgtt gtccccccggg gagtcagagc atctgctgga accggcagaa 1000
gctgaaaggt ctcagaggag gaggctgctg gttccagcaa atgaaggtga 1050
tcccactgag actctgagac agtgcttcga tgactttgca gacttggtgc 1100
cctttgactc ctgggagccg ctcatgagga agttgggcct catggacaat 1150
gagataaagg tggctaaagc tgaggcagcg ggccacaggg acaccccttgc 1200
cacgatgctg ataaagtggg tcaacaaaac cgggcgagat gcctctgtcc 1250
acaccctgct ggatgccttg gagacgctgg gagagagact tgccaaagcag 1300

aagattgagg accacttgtt gagctctgga aagttcatgt atctagaagg 1350
taatgcagac tctgccwtgt cctaagtgtg attctcttca ggaagtgaga 1400
ccttccctgg ttacaccccttt ttctggaaaaa agcccaactg gactccagtc 1450
agtaggaaag tgccacaatt gtcacatgac cggtactgga agaaaactctc 1500
ccatccaaca tcacccagtg gatggaacat cctgtaactt ttcactgcac 1550
ttggcattat tttataaagc tgaatgtgat aataaggaca ctatggaaat 1600
gtctggatca ttccgtttgt gcgtactttg agattggtt tggatgtca 1650
ttgtttcac agcactttt tattctaatg taaatgcttt atttatttat 1700
ttgggctaca ttgtaagatc catctacaaa aaaaaaaaaaa aaaaaaaaaag 1750
ggcggccgcg actctagagt cgacctgcag aagcttggcc gccatggcc 1799

<210> 11
<211> 411
<212> PRT
<213> Homo sapiens

<220>
<221> Unsure
<222> 410
<223> Xaa may be leucine or methionine

<400> 11
Met Glu Gln Arg Gly Gln Asn Ala Pro Ala Ala Ser Gly Ala Arg
1 5 10 15
Lys Arg His Gly Pro Gly Pro Arg Glu Ala Arg Gly Ala Arg Pro
20 25 30
Gly Leu Arg Val Pro Lys Thr Leu Val Leu Val Val Ala Ala Val
35 40 45
Leu Leu Leu Val Ser Ala Glu Ser Ala Leu Ile Thr Gln Gln Asp
50 55 60
Leu Ala Pro Gln Gln Arg Ala Ala Pro Gln Gln Lys Arg Ser Ser
65 70 75
Pro Ser Glu Gly Leu Cys Pro Pro Gly His His Ile Ser Glu Asp
80 85 90
Gly Arg Asp Cys Ile Ser Cys Lys Tyr Gly Gln Asp Tyr Ser Thr
95 100 105

His Trp Asn Asp Leu Leu Phe Cys Leu Arg Cys Thr Arg Cys Asp
110 115 120

Ser Gly Glu Val Glu Leu Ser Pro Cys Thr Thr Thr Arg Asn Thr
125 130 135

Val Cys Gln Cys Glu Glu Gly Thr Phe Arg Glu Glu Asp Ser Pro
140 145 150

Glu Met Cys Arg Lys Cys Arg Thr Gly Cys Pro Arg Gly Met Val
155 160 165

Lys Val Gly Asp Cys Thr Pro Trp Ser Asp Ile Glu Cys Val His
170 175 180

Lys Glu Ser Gly Ile Ile Ile Gly Val Thr Val Ala Ala Val Val
185 190 195

Leu Ile Val Ala Val Phe Val Cys Lys Ser Leu Leu Trp Lys Lys
200 205 210

Val Leu Pro Tyr Leu Lys Gly Ile Cys Ser Gly Gly Gly Asp
215 220 225

Pro Glu Arg Val Asp Arg Ser Ser Gln Arg Pro Gly Ala Glu Asp
230 235 240

Asn Val Leu Asn Glu Ile Val Ser Ile Leu Gln Pro Thr Gln Val
245 250 255

Pro Glu Gln Glu Met Glu Val Gln Glu Pro Ala Glu Pro Thr Gly
260 265 270

Val Asn Met Leu Ser Pro Gly Glu Ser Glu His Leu Leu Glu Pro
275 280 285

Ala Glu Ala Glu Arg Ser Gln Arg Arg Arg Leu Leu Val Pro Ala
290 295 300

Asn Glu Gly Asp Pro Thr Glu Thr Leu Arg Gln Cys Phe Asp Asp
305 310 315

Phe Ala Asp Leu Val Pro Phe Asp Ser Trp Glu Pro Leu Met Arg
320 325 330

Lys Leu Gly Leu Met Asp Asn Glu Ile Lys Val Ala Lys Ala Glu
335 340 345

Ala Ala Gly His Arg Asp Thr Leu Tyr Thr Met Leu Ile Lys Trp
350 355 360

Val Asn Lys Thr Gly Arg Asp Ala Ser Val His Thr Leu Leu Asp
365 370 375

Ala Leu Glu Thr Leu Gly Glu Arg Leu Ala Lys Gln Lys Ile Glu
380 385 390

Asp His Leu Leu Ser Ser Gly Lys Phe Met Tyr Leu Glu Gly Asn
395 400 405

Ala Asp Ser Ala Xaa Ser
410

<210> 12

<211> 29

<212> DNA

<213> Homo sapiens

<400> 12

atcaggact ttccgctggg gactttccg 29

<210> 13

<211> 30

<212> DNA

<213> Homo sapiens

<400> 13

aggatggaa gtgtgtata tattcattat 30

<210> 14

<211> 418

<212> PRT

<213> Homo sapiens

<400> 14

Gly Arg Gly Ala Leu Pro Thr Ser Met Gly Gln His Gly Pro Ser
1 5 10 15

Ala Arg Ala Arg Ala Gly Arg Ala Pro Gly Pro Pro Pro Ala Arg
20 25 30

Glu Ala Ser Pro Arg Leu Arg Val His Lys Thr Phe Lys Phe Val
35 40 45

Val Val Gly Val Leu Leu Gln Val Val Pro Ser Ser Ala Ala Thr
50 55 60

Ile Lys Leu His Asp Gln Ser Ile Gly Thr Gln Gln Trp Glu His
65 70 75

Ser Pro Leu Gly Glu Leu Cys Pro Pro Gly Ser His Arg Ser Glu

80	85	90
Arg Pro Gly Ala Cys Asn Arg Cys Thr Glu	Gly Val Gly Tyr Thr	
95	100	105
Asn Ala Ser Asn Asn Leu Phe Ala Cys Leu	Pro Cys Thr Ala Cys	
110	115	120
Lys Ser Asp Glu Glu Glu Arg Ser Pro Cys	Thr Thr Thr Arg Asn	
125	130	135
Thr Ala Cys Gln Cys Lys Pro Gly Thr Phe	Arg Asn Asp Asn Ser	
140	145	150
Ala Glu Met Cys Arg Lys Cys Ser Thr Gly	Cys Pro Arg Gly Met	
155	160	165
Val Lys Val Lys Asp Cys Thr Pro Trp Ser	Asp Ile Glu Cys Val	
170	175	180
His Lys Glu Ser Gly Asn Gly His Asn Ile	Trp Val Ile Leu Val	
185	190	195
Val Thr Leu Val Val Pro Leu Leu Leu Val	Ala Val Leu Ile Val	
200	205	210
Cys Cys Cys Ile Gly Ser Gly Cys Gly	Gly Asp Pro Lys Cys Met	
215	220	225
Asp Arg Val Cys Phe Trp Arg Leu Gly Leu	Leu Arg Gly Pro Gly	
230	235	240
Ala Glu Asp Asn Ala His Asn Glu Ile	Leu Ser Asn Ala Asp Ser	
245	250	255
Leu Ser Thr Phe Val Ser Glu Gln Gln	Met Glu Ser Gln Glu Pro	
260	265	270
Ala Asp Leu Thr Gly Val Thr Val Gln	Ser Pro Gly Glu Ala Gln	
275	280	285
Cys Leu Leu Gly Pro Ala Glu Ala Glu	Gly Ser Gln Arg Arg Arg	
290	295	300
Leu Leu Val Pro Ala Asn Gly Ala Asp Pro	Thr Glu Thr Leu Met	
305	310	315
Leu Phe Phe Asp Lys Phe Ala Asn Ile Val	Pro Phe Asp Ser Trp	
320	325	330
Asp Gln Leu Met Arg Gln Leu Asp Leu Thr	Lys Asn Glu Ile Asp	

335

340

345

Val Val Arg Ala Gly Thr Ala Gly Pro Gly Asp Ala Leu Tyr Ala
350 355 360

Met Leu Met Lys Trp Val Asn Lys Thr Gly Arg Asn Ala Ser Ile
365 370 375

His Thr Leu Leu Asp Ala Leu Glu Arg Met Glu Glu Arg His Ala
380 385 390

Lys Glu Lys Ile Gln Asp Leu Leu Val Asp Ser Gly Lys Phe Ile
395 400 405

Tyr Leu Glu Asp Gly Thr Gly Ser Ala Val Ser Leu Glu
410 415

<210> 15

<211> 74

<212> PRT

<213> Homo sapiens

<400> 15

Val Met Asp Ala Val Pro Ala Arg Arg Trp Lys Glu Phe Val Arg
1 5 10 15

Thr Leu Gly Leu Arg Glu Ala Glu Ile Glu Ala Val Glu Val Glu
20 25 30

Ile Gly Arg Phe Arg Asp Gln Gln Tyr Glu Met Leu Lys Arg Trp
35 40 45

Arg Gln Gln Gln Pro Ala Gly Leu Gly Ala Val Tyr Ala Ala Leu
50 55 60

Glu Arg Met Gly Leu Asp Gly Cys Val Glu Asp Leu Arg Ser
65 70

<210> 16

<211> 78

<212> PRT

<213> Homo sapiens

<400> 16

Val Val Glu Asn Val Pro Pro Leu Arg Trp Lys Glu Phe Val Arg
1 5 10 15

Arg Leu Gly Leu Ser Asp His Glu Ile Asp Arg Leu Glu Leu Gln
20 25 30

Asn Gly Arg Cys Leu Arg Glu Ala Gln Tyr Ser Met Leu Ala Thr

35

40

45

Trp Arg Arg Arg Thr Pro Arg Arg Glu Ala Thr Leu Glu Leu Leu
50 55 60

Gly Arg Val Leu Arg Asp Met Asp Leu Leu Gly Cys Leu Glu Asp
65 70 75

Ile Glu Glu

<210> 17

<211> 77

<212> PRT

<213> Homo sapiens

<400> 17

Ile Ala Gly Val His Thr Leu Ser Gln Val Lys Gly Phe Val Arg
1 5 10 15

Lys Asn Gly Val Asn Glu Ala Lys Ile Asp Glu Ile Lys Asn Asp
20 25 30

Asn Val Gln Asp Thr Ala Glu Gln Lys Val Gln Leu Leu Arg Asn
35 40 45

Trp His Gln Leu His Gly Lys Lys Glu Ala Tyr Asp Thr Leu Ile
50 55 60

Lys Asp Leu Lys Lys Ala Asn Leu Cys Thr Leu Ala Glu Lys Ile
65 70 75

Gln Thr